



#12

SEQUENCE LISTING

<110> NITROGEN, Geoffrey

<120> METHOD OF TREATMENT AND AGENTS USEFUL
FOR SAME

<130> DAVI103.001AUS

<140> 09/632,074

<141> 2000-08-02

<150> AU/PQ/1999

<151> 1999-08-03

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 504

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)... (504)

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atg cat tgg gga acc ctg tgc gga ttc ttg tgg ctt tgg ccc tat ctt	48
Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu	
1 5 10 15	

ttc tat gtc caa gct gtg ccc atc caa aaa gtc caa gat gac acc aaa	96
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys	
20 25 30	

acc ctc atc aag aca att gtc acc agg atc aat gac att tca cac acg	144
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr	
35 40 45	

cag tca gtc tcc tcc aaa cag aaa gtc acc ggt ttg gac ttc att cct	192
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro	
50 55 60	

ggg ctc cac ccc atc ctg acc tta tcc aag atg gac cag aca ctg gca	240
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala	
65 70 75 80	

gtc tac caa cag atc ctc acc agt atg cct tcc aga aac gtg atc caa	288
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln	
85 90 95	

ata tcc aac gac ctg gag aac ctc cgg gat ctt ctt cac gtg ctg gcc	336
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Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala		
			100					105					110				
ttc	tct	aag	agc	tgc	cac	ttg	ccc	tgg	gcc	agt	ggc	ctg	gag	acc	ttg	384	
Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu		
		115					120					125					
gac	agc	ctg	ggg	ggg	gtc	ctg	gaa	gct	tca	ggc	tac	tcc	aca	gag	gtg	432	
Asp	Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val		
		130					135				140						
gtg	gcc	ctg	agc	agg	ctg	cag	ggg	tct	ctg	cag	gac	atg	ctg	tgg	cag	480	
Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln		
		145				150				155					160		
ctg	gac	ctc	agc	cct	ggg	tgc	tga									504	
Leu	Asp	Leu	Ser	Pro	Gly	Cys	*										
				165													

<210> 2
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 2

Met	His	Trp	Gly	Thr	Leu	Cys	Gly	Phe	Leu	Trp	Leu	Trp	Pro	Tyr	Leu		
1				5				10						15			
Phe	Tyr	Val	Gln	Ala	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys		
		20					25					30					
Thr	Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr		
		35				40					45						
Gln	Ser	Val	Ser	Ser	Lys	Gln	Lys	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro		
	50				55					60							
Gly	Leu	His	Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala		
65			70					75						80			
Val	Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Ile	Gln		
		85				90							95				
Ile	Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala		
		100				105						110					
Phe	Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu		
		115				120						125					
Asp	Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val		
	130				135					140							
Val	Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln		
145				150				155							160		
Leu	Asp	Leu	Ser	Pro	Gly	Cys											
				165													

<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
<223> GAPDH forward primer.

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cagtcagccg catcttcttt tg 22

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> GAPDH backward primer.

<400> 4
tggttcacac ccatgacgaa c 21

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> OPG forward primer.

<400> 5
gtacgtcaag caggagtgca atc 23

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> OPG backward primer.

<400> 6
ttcttgtgag ctgtgttgcc g 21

<210> 7
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<212> DNA
<213> Artificial Sequence

<220>
<223> RANK forward primer.

<400> 7
ttaagccagt gcttcacggg 20

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> RANK backward primer.

<400> 8
acgtagacca cgatgatgtc gc

22